IN THE CLAIMS:

1. (Currently amended) A method for determining the likelihood that a human patient suspected of SMEI does or does not have SMEI comprising:

(1) screening a patient sample for the existence of ~~an alteration~~ a mutation in the SCN1A gene of the patient, including in a regulatory region of the gene, by sequencing the SCN1A gene;

(2) (a) terminating the process if no ~~alteration~~ mutation is found~~, thereby establishing that the patient likely does not have SMEI~~; or

(b) identifying the ~~alteration~~ mutation; and

(3) ascertaining whether the ~~alteration~~ mutation, when one is detected, has previously been detected in a patient clinically diagnosed with SMEI and is therefore considered SMEI associated or has previously been detected in a patient ~~not diagnosed with~~ unaffected by SMEI and is therefore considered non-SMEI associated, or [[is]] if not considered to be either, (i) considering genetic data for the parents of the patient and establishing whether the mutation has arisen *de novo* or is inherited; and (ii) establishing whether the mutation is a truncating mutation; wherein

(a) the patient is categorized as having a very high probability of having SMEI when the ~~alteration~~ mutation is SMEI associated;

(b) the patient is categorized as having a low probability of having SMEI when the ~~alteration~~ mutation is non-SMEI associated; or

(c) the patient is categorized as having a low probability of SMEI in the case of an inherited mutation, a high probability of SMEI in the case of a *de novo* mutation, and a very high probability of SMEI in the case of a *de novo* mutation which is truncating ~~further analysis is undertaken to establish the likelihood the patient suspected of SMEI does or does not have SMEI when the detected alteration is not considered to be either SMEI associated or non-SMEI associated,~~

~~wherein the detection of a SMEI associated alteration establishes that a patient suspected of SMEI likely does have SMEI~~.

2-25. (Canceled)

Please add the following new claims:

26. (New) A method for determining the likelihood that a human patient suspected of SMEI does or does not have SMEI, the method comprising:

(1) screening a patient sample for the existence of a mutation in the SCN1A gene of the patient, by sequencing the SCN1A gene;

(2) (a) terminating the process if no mutation is found; or
(b) identifying the mutation; and

(3) ascertaining whether the mutation, when one is detected, has previously been detected in a patient clinically diagnosed with SMEI and is therefore considered SMEI associated or has previously been detected in a patient unaffected by SMEI and is therefore considered non-SMEI associated, or if not considered to be either, (i) considering genetic data for the parents of the patient and establishing whether the mutation has arisen *de novo* or is inherited; and (ii) establishing whether the mutation is a truncating mutation; wherein

(a) the patient is categorized as having a very high probability of having SMEI when the mutation is SMEI associated;

(b) the patient is categorized as having a low probability of having SMEI when the mutation is non-SMEI associated; or

(c) the patient is categorized as having a low probability of SMEI in the case of an inherited mutation, a high probability of SMEI in the case of a *de novo* mutation, and a very high probability of SMEI in the case of a *de novo* mutation which is truncating.

27. (New) The method of claim 1, further comprising generating and outputting to a user computer generated chromatograms indicating the likelihood that a human patient suspected of SMEI does or does not have SMEI.